REMARKS

The brief description of Figures 1-5 has been amended to provide sequence identification numbers. The partial paragraph covering page 7 has been amended to delete the hyperlink reference (http://). Pages 5 and 15 have been amended to insert sequence identification numbers.

Claims 1, 7, 13, and 15-28 are pending in the present application. By the present amendment, claims 1 and 19 have been amended. New claims 29-38 have been added, support for which can be found at, for example, page 2, line 21 to page 3, line 9; page 6, lines 9-17; and page 11, lines 7-16 of the specification. No new matter has been added. Upon entry of the present amendment, claims 1, 7, 13 and 15-38 will be pending.

Applicants request that the Patent and Trademark Office acknowledge receipt and consideration of the Information Disclosure Statements that were filed on May 7, 2001, June 4, 2001, July 9, 2001, August 7, 2001, in the present application. In particular, it is requested that the Examiner sign the submitted Forms 1449 and return a copy of each signed page.

I. The Requirement For Restriction Is Unwarranted

The Office action presents two issues regarding the requirement for restriction. First, there allegedly is no single special technical feature linking the recombinant nucleic acid molecules of Group I (claims 1, 7, 13, 15-23, and 25-28) with the method of isolating a promoter of Group II (claim 24). Second, each of SEQ ID NOs 15, 16, 17, and 18 are to be treated as separate and distinct inventions subject to a restriction requirement and not as species subject to an election of species. Applicants affirm the election of the claims of Group I and SEQ ID NO:15 with traverse, and respectfully request reconsideration of the same.

In regard to the first issue, the Office action asserts that the claims of Group I and Group II are not linked by a single special technical feature because the invention of Group I does not constitute an advance over the prior art. The requirement of unity of invention, which applies in the present national stage application, is fulfilled when there is a technical relationship among those inventions involving one or more of the same or corresponding special technical features

that define a contribution that each of the claimed inventions, considered as a whole, makes over the prior art. One special technical feature shared by the claims of Group I and the claim of Group II is, for example, a promoter sequence that hybridizes to nucleic acid molecule having a sequence of any of SEQ ID NOs 15, 16, 17, or 18, or a complement thereof. The only prior art referred to in the Office action is Singh *et al.*, *Plant Science*, **1997**, *130*, 189-196. Curiously, the Office action fails to point out where the Singh reference discloses this special technical feature. Thus, the Office action has not met its burden. Accordingly, claim 24 should be included within Group I.

Regarding the second issue, simply because each of SEQ ID NOs 15, 16, 17, and 18 may be treated as separate and distinct inventions does not necessarily subject them to a restriction requirement. M.P.E.P. § 803.04 is instructive:

> Nucleotide sequences encoding different proteins are structurally distinct chemical compounds and are unrelated to one another. These sequences are thus deemed to normally constitute independent and distinct inventions within the meaning of 35 U.S.C. 121. Absent evidence to the contrary, each such nucleotide sequence is presumed to represent an independent and distinct invention, subject to a restriction requirement pursuant to 35 U.S.C. 121 and 37 CFR 1.141 et seq. Nevertheless, to further aid the biotechnology industry in protecting its intellectual property without creating an undue burden on the Office, the Commissioner has declared *sua sponte* to partially waive the requirements of 37 CFR 1.141 et seq. and permit a reasonable number of such nucleotide sequences to be claimed in a single application. See Examination of Patent Applications Containing Nucleotide Sequences, 1192 O.G. 68 (November 19, 1996).
>
> It has been determined that normally ten sequences constitute a reasonable number for examination purposes. Accordingly, in most cases, up to ten independent and distinct nucleotide sequences will be examined in a single application without restriction.

Thus, because there are only four sequences (i.e., SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, and SEQ ID NO:18) that are alleged to be independent and distinct, they can easily be combined in a single application without creating an undue burden on the Office to further aid the biotechnology industry in protecting its intellectual property. Certainly, these four sequences constitute a reasonable number of such nucleotide sequences to be claimed in a single application.

In view of the foregoing, Applicants submit that all pending claims should be examined in the same application without restriction.

II. The Claims Are Clear and Definite

Claims 1, 19, and 25 are rejected under 35 U.S.C. § 112, second paragraph, as allegedly being indefinite for failing to particularly point out and distinctly claim the subject matter which Applicants regard as the invention. Applicants traverse the rejection and respectfully requests reconsideration because the claims are clear and definite.

Claim 1 is alleged to be indefinite in reciting "mediating." The Office action asserts that it is not clear how "mediating" affects seed-specific expression. Although Applicants submit that one skilled in the art would understand what is meant by the term "mediating," particularly in the context in which it is used, Applicants have amended claim 1 to recite "directing." Applicants teach at, for example, page 1, lines 11-13 of the specification, upstream DNA sequences "directing" expression of proteins. Applicants submit that the term "directing" is clearer than the term "specifying," which was suggested in the Office action. Claim 1 has not been narrowed by this amendment.

Claims 1 and 25 are alleged to be indefinite in reciting "stringent conditions" because the specification fails to provide a definition. Contrary to the assertions in the Office action, Applicants have provided a definition of "stringent conditions" in the specification at, for example, page 8, lines 5-20. The Office action fails to explain why such a definition is deficient. Indeed, persons of ordinary skill would have no difficulty in determining whether a particular hybridization meets these criteria. Accordingly, the claims are definite within the meaning of § 112. *In re Mercier*, 185 U.S.P.Q. 774 (C.C.P.A. 1975) (claims sufficiently define an invention so long as one skilled in the art can determine what subject matter is or is not within the scope of the claims).

The Office action alleges that claim 19 is indefinite in reciting "under conditions" and suggests deleting the same from the claim. Although Applicants submit that claim 19 is definite as written, to advance prosecution of the present application, claim 19 has been amended accordingly. Claim 19 has not been narrowed.

In view of the forgoing, the claims are clear and definite. Accordingly, Applicants respectfully request that the rejection under 35 U.S.C. § 112, second paragraph be withdrawn.

III. The Claimed Inventions Are Supported by Ample Written Description

Claims 1, 7, 13, and 15-25 are rejected under 35 U.S.C. §112, first paragraph, as allegedly containing subject matter that was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor, at the time the application was filed, had possession of the claimed invention. Applicants traverse the rejection and respectfully request reconsideration because the specification provides ample written description supporting the claimed inventions.

The Office action asserts that Applicants do not identify structural features unique to the 393 base pair fragment from the *Arabidopsis* FAE1 promoter of SEQ ID NO:15. The Office action further asserts that, referring to *University of California v. Eli Lilly and Co.*, 43 U.S.P.Q.2d 1398 (Fed. Cir. 1997), given the lack of structural features for the *Arabidopsis* FAE1 promoter, it is unclear what "features identify a 393 bp fragment from *Arabidopsis* FAE1 promoter, including a *Arabidopsis* FAE1 promoter with 70% homology to SEQ ID NO:15 or any sequence that hybridizes under stringent conditions to SEQ ID NO:15." Applicants submit that identification of structural features unique to the 393 base pair fragment from the *Arabidopsis* FAE1 promoter of SEQ ID NO:15 is not necessary to provide an adequate written description of the claimed invention, nor is it required by *University of California v. Eli Lilly and Co.* As stated in the "Guidelines for Examination of Patent Applications Under the 35 U.S.C. 112, para. 1 'Written Description' Requirement,":

> Possession may be shown in a variety of ways including description of an actual reduction to practice, or by showing that the invention was "ready for patenting" such as by the disclosure of drawings or structural chemical formulas that show that the invention was complete, or by describing distinguishing identifying characteristics sufficient to show that the applicant was in possession of the claimed invention.

In accordance with these standards, Applicants have indeed described distinguishing identifying characteristics sufficient to show that the Applicants were in possession of the claimed invention. The pending claims recite recombinant nucleic acid molecules wherein, *inter alia*, the

transcriptional regulatory region hybridizes under stringent conditions to a sequence selected from the group consisting of SEQ ID NO:15, 16, 17, and 18, or the complement thereof (e.g., claim 1). Alternately, the pending claims recite recombinant nucleic acid molecules wherein, *inter alia*, the promoter sequence is at least 70% or 80% identical to a sequence selected from the group consisting of SEQ ID NO:15, 16, 17, and 18, or the complement thereof (e.g., claims 7 and 22). Thus, each of the pending claims recites a specific nucleotide sequence (i.e., a distinguishing identifying characteristic) in the context of either stringent hybridization with or identity thereto. Applicants teach appropriate parameters for determining both stringent hybridization conditions (at, for example, page 8, lines 5-20 of the specification) and identity (at, for example, page 7, line 1 to page 8, line 4 of the specification). A specific nucleotide sequence is clearly a distinguishing identifying characteristic sufficient to show that the Applicants were in possession of the claimed invention.

In addition, the written description provided in Applicants' specification fully complies with *University of California v. Eli Lilly and Co.*, which states:

> Thus, as we have previously held, a cDNA is not defined or described by the mere name "cDNA," even if accompanied by the name of the protein that it encodes, but requires a kind of specificity usually achieved by means of the recitation of the sequence of nucleotides that make up the cDNA.

Id. at 1406. Indeed, as argued above, Applicants have provided the ultimate written description of the claimed invention – the nucleotide sequence.

Thus, in view of the foregoing, Applicants have provided adequate written description of the invention describing sufficient distinguishing identifying characteristics. Accordingly, Applicants respectfully request that the rejection under 35 U.S.C. §112, first paragraph, as allegedly failing to provide sufficient written description be withdrawn. If the present rejection is maintained, Applicants request that the examiner particularly point out exactly which portion of a particular claim is allegedly not described.

IV. The Claimed Invention Is Sufficiently Enabled

A. Claim 19

Claim 19 is rejected under 35 U.S.C. § 112, first paragraph as allegedly failing to provide an enabling disclosure. The Office action mistakenly asserts that it would require undue experimentation for one skilled in the art to alter the phenotype of a seed by transforming a seed-bearing plant with a vector comprising the nucleic acid molecule of claim 1. Applicants traverse the rejection and respectfully requests reconsideration because one skilled in the art would be able to practice the claimed invention without being required to perform undue experimentation.

As will be recognized, the enablement requirement of §112 is satisfied so long as a disclosure contains sufficient information that persons of ordinary skill in the art having the disclosure before them would be able to make and use the invention. *In re Wands*, 8 U.S.P.Q.2d 1400 (Fed. Cir. 1988) (the legal standard for enablement under §112 is whether one skilled in the art would be able to practice the invention without undue experimentation). In this respect, the following statement from *In re Marzocchi*, 169 U.S.P.Q. 367, 369-370 (C.C.P.A. 1971), is noteworthy:

> The only relevant concern of the Patent Office under these circumstances should be over the truth of any such assertion. The first paragraph of §112 requires nothing more than objective enablement. How such a teaching is set forth, either by the use of illustrative examples or by broad terminology, is of no importance.
>
> As a matter of Patent Office practice, then, a specification disclosure which contains a teaching of the manner and process of making and using the invention in terms which correspond in scope to those used in describing and defining the subject matter sought to be patented **must** be taken as in compliance with the enabling requirements of the first paragraph of §112 unless there is reason to doubt the objective truth of the statements contained therein which must be relied upon for enabling support. (emphasis added)

Any assertion by the Patent Office that an enabling disclosure is not commensurate in scope with the protection sought must be supported by evidence or reasoning substantiating the doubts so expressed. *In re Dinh-Nguyen*, 181 U.S.P.Q. 46 (C.C.P.A. 1974); *In re Bowen*, 181 U.S.P.Q. 48 (C.C.P.A. 1974). The only reasoning provided in the Office action is that plant transformation is unpredictable. In support of this assertion, the Office action cites two references, which purport

results using different transformation systems with different promoters and different inserted nucleic acid molecules.

The Office action ignores the illustrative examples provided in the specification. Applicants teach at, for example, pages 12-16 of the specification, methods of altering the phenotype of a seed by transformation with a nucleic acid molecule of claim 1. Indeed, Applicants teach at page 13, lines 16-19 that:

> Both the 934 bp and the 393 bp transcriptional regulatory regions derived from the *A.t.* FAE1 gene caused the appearance of GUS activity by the torpedo stage embryo (6 days after flowering). GUS activity in all five lines persisted throughout subsequent embryo development.

In addition, similar transcriptional regulatory regions from different species of plant also yielded alteration of seed phenotype upon transformation (see, the working example on pages 14-16 of the specification). Thus, given the explicit working example provided in the specification, there can be no question that one skilled in the art would be able to practice the method of claim 19 without being required to perform any amount of undue experimentation.

In view of the forgoing, there is no reason to believe that one skilled in the art would be required to perform any amount of undue experimentation in order to make and use the claimed invention. Accordingly, Applicants respectfully request that the rejection under 35 U.S.C. § 112, first paragraph be withdrawn.

B. Claims 1, 7, 13, and 15-25

Claims 1, 7, 13, and 15-25 are rejected under 35 U.S.C. § 112, first paragraph as allegedly failing to provide an enabling disclosure. The Office action recognizes that the specification enables one skilled in the art to use 393 bp regions from the *Arabidopsis* FAE1 promoter to obtain seed-specific expression of a GUS reporter gene in *Arabidopsis*. The Office action, however, mistakenly asserts that it would require undue experimentation for one skilled in the art to use sequences that hybridize under stringent conditions to SEQ ID NO:15, or sequences that are 70% to 80% identical to SEQ ID NO:15. Applicants traverse the rejection and respectfully requests reconsideration because one skilled in the art would be able to practice the claimed invention without being required to perform undue experimentation.

As stated above, Applicants provide examples demonstrating alteration of the phenotype of a seed using both a 393 bp region and a 934 bp region of the *Arabidopsis* FAE1 promoter. One skilled in the art would be able to use additional promoter regions that are either 70-80% identical to SEQ ID NO:15 or hybridize to SEQ ID NO:15 under stringent conditions to alter the phenotype of a seed upon transformation. One skilled in the art would also be able to use additional promoter regions that are either 70-80% identical to SEQ ID NO:16, 17, or 18, or hybridize to SEQ ID NO:16, 17, or 18, under stringent conditions to alter the phenotype of a seed upon transformation. No amount of undue experimentation is required to make any nucleic acid molecule having these features. For example, one skilled in the art can, without performing any amount of undue experimentation, make any one or all of the nucleic acid molecules that are at least 70% identical to, for example, SEQ ID NO:15. In addition, one skilled in the art can also make any one or all of the nucleic acid molecules that would hybridize under stringent conditions to, for example, SEQ ID NO:15, without performing any amount of undue experimentation. The Office action does not appear to dispute this. Indeed, the Office action fails to provide any reasoning why one skilled in the art could not make the recombinant nucleic acid molecules within the scope of claim 1.

What the Office action appears to assert is that it would require undue experimentation for one skilled in the art to **predict** which recombinant nucleic acid molecule that is either at least 70% identical to SEQ ID NO:15 or hybridizes to SEQ ID NO:15 under stringent conditions would alter the phenotype of a seed upon transformation. Applicants submit that no prediction is necessary. Indeed, one skilled in the art would simply assess the activity of a particular recombinant nucleic acid molecule in the same manner as taught in the specification for the nucleic acid molecules comprising the 393 bp region and a 934 bp region of the *Arabidopsis* FAE1 promoter. The Office action cites several references that show the relevance, to varying degrees, of particular regions of a promoter in their ability to direct gene expression. These references serve to show the level of skill in the art in designing promoter regions that can be used to effectively direct gene expression. Applicants remind the examiner that Applicants are not claiming just a promoter but, rather, a promoter that comprises a "transcriptional regulatory region capable of mediating seed-specific expression in *Arabidopsis*." Applicants clearly teach one skilled in the art how to assay for such activity. No amount of undue experimentation is required to test other recombinant nucleic acid molecules for the same activity.

In view of the forgoing, there is no reason to believe that one skilled in the art would be required to perform any amount of undue experimentation in order to make and use the claimed invention. Accordingly, Applicants respectfully request that the rejection under 35 U.S.C. § 112, first paragraph be withdrawn.

V. Conclusion

In view of the foregoing, Applicants respectfully submit that the claims are in condition for allowance. An early notice of the same is earnestly solicited. The examiner is invited to contact Applicants' undersigned representative at (503) 226-7391 if there are any questions regarding Applicants' claimed invention. Attached hereto is a marked-up version of the changes made to the specification and claims by the current amendment. The attached page is captioned **Version with Markings to Show Changes Made**.

Respectfully submitted,

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification:

The paragraph commencing at page 2, line 15 is amended as follows:

Figure 1 shows a 934 bp DNA sequence (SEQ ID NO:16) comprising the *Arabidopsis thaliana FAE1* transcription regulatory sequence.

The paragraph commencing at page 2, line 17 is amended as follows:

Figure 2 shows a 1588 bp DNA sequence (SEQ ID NO:17) comprising the *Brassica napus FAE1* transcription regulatory sequence.

The paragraph commencing at page 2, line 19 is amended as follows:

Figure 3 shows a 1069 bp DNA sequence (SEQ ID NO:18) comprising the *Lunaria annua FAE1* transcription regulatory sequence.

The partial paragraph at page 2, lines21-33 is amended as follows:

Figure 4 shows an alignment of the *Arabidopsis thaliana (A.t.)* (SEQ ID NO:19), *Lunaria annua (L.a.)* (SEQ ID NO:21) and *Brassica napus (B.n.)* (SEQ ID NO:20) transcription regulatory sequences. Asterisks below the sequences indicate identical nucleotides in each of the three sequences. A number of putative cis-acting sequence motifs are identified in the *A. thaliana* sequence: an EMl ABA box at -44bp to -36bp having the sequence ACATCTCAT, for which the published consensus sequence is ACGTGTCAT (Rowley, D.L. and Herman, E.M. (1997), Biochimica et Biophysica Acta 1345:1-4); an A-300 box at -51bp to -46bp having the sequence TGCAAT, for which the published consensus sequence is TG(T/A/C)AAA(G/T) (Morton et al. (1994) in Seed Development and Germination (Kigel, J. and Gallili, G., eds.) pp. 103-138, Marcel Dekker, New York); G-box 1 at -105 to -100 bp having the sequence CACATG, for which is the consensus sequence is CACCTG, and G-box 2 at -164 to -159 bp having the sequence CAACTT, for which the consensus sequence is CAACTG (Kawogoe, Y. and Murai, N. (1992) Plant J. 2:927-936; CEl element at -226 to -218 bp having the sequence

The partial paragraph at page 3, lines 1-9 is amended as follows:

TTCCATCGA, for which the consensus sequence is TGCCACCGG, and a CE3 element at -381 bp to -369 bp having the sequence ACACATTCCCTC (SEQ ID NO:1), for which the consensus

sequence is ACGCGTGTCCTC (SEQ ID NO:2) (Shen et al., (1996) Plant Cell 8:1107-1119). Not highlighted is a putative RY repeat motif at -53bp to -47bp having the sequence CATGCAA, for which the consensus sequence is CATGCAT (Dickinson et al. (1988) Nucleic Acid Res. 16:371; Lelievre et al. (1992) Plant Physiol. 98:387-391). Also shown, as Con. 4, is a consensus sequence (SEQ ID NO:22), wherein R=G or A, Y=T/U or C, M=A or C, K=G or T/U, S=G or C, W=A or T/U, B=G or C or T/U, D=A or G or T/U, H=A or C or T/U, V=A or G or C and N=A or G or C or T/U.

The paragraph commencing at page 3, line 10 is amended as follows:

Figure 5 shows an alignment of the *Arabidopsis thaliana (A.t.)* and *Lunaria annua (L.a.)* transcription regulatory sequences. Asterisks below the sequences indicate identical nucldeotides in each of the two sequences. The base at position -400 in the *A.t.* sequence is highlighted. The alignment of sequences in both Figure 4 and Figure 5 was accomplished using the CLUSTALW program (version 1.74) for multiple sequence alignments, using a gap open penalty of 15, a gap extension penalty of 6.66 and an IUB DNA weight matrix. Also shown, as Con. 5, is a consensus sequence (SEQ ID NO:23), wherein R=G or A, Y=T/U or C, M=A or C, K=G or T/U, S=G or C, W=A or T/U, B=G or C or T/U, D=A or G or T/U, H=A or C or T/U, V=A or G or C and N=A or G or C or T/U.

The partial paragraph at page 7, lines 1-33 is amended as follows:

Optimal alignment of sequences for comparisons of similarity may be automated using a variety of algorithms, such as the local homology algorithm of Smith and Waterman (1981) *Adv. Appl. Math* 2:482, the homology alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443, the search for similarity method of Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. USA* 85:2444, and the computerized implementations of these algorithms (such as GAP, BESTFIT, FASTA and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, Madison, WI, U.S.A.). sequence similarity may also be determined using the BLAST algorithm, described in Altschul *et al.* (1990), *J. Mol. Biol.* 215:403-10 (using the published default settings). Software and instructions for performing BLAST analysis may be available through the National Center for Biotechnology Information in the United States (including the programs BLASTP, BLASTN, BLASTX, TBLASTN and TBLASTX that may be available through the internet at [http://] www.ncbi.nlm.nih.gov/. The BLAST algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of

length W in the query sequence that either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database (reference) sequence. T is referred to as the neighborhood word score threshold. Initial neighborhood word hits act as seeds for initiating searches to find longer HSPs. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Extension of the word hits in each direction is halted when the following parameters are met: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T and X determine the sensitivity and speed of the alignment. The BLAST program may use as defaults a word length (W) of ll, the BLOSUM62 scoring matrix (Henikoff and Henikoff (1992) *Proc. Natl. Acad. Sci. USA* 89:10915-10919), a gap existence cost of 11, a per residue gap cost of 1, a lambda ratio of 0.85, alignments (B) of 50, expectation (E) of 10, M=5, N=4, and a comparison of both strands. One measure of the statistical similarity between two sequences using the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. In alternative embodiments of the invention, nucleotide or amino acid sequences are considered substantially identical if the smallest sum probability in a comparison of the test sequences is less than about 1, preferably less than about 0.1, more preferably less than

The paragraph commencing at page 12, line 1 is amended as follows:

Using the sequence information of the *A. thaliana* genome sequencing project, synthetic oligonucleotide primers were designed to amplify the *FAE1* 5' untranslated region, to isolate it by PCR. As shown in Figure 1, the upstream primer 5'-CTAGTAGATTGGTTGGTTGGTTTCC-3' (AtproFW) (SEQ ID NO:3) in combination with the downstream primer 5'-TGCTCTGTTTGTGTCGGAAAATAATGG-3' (AtproRV) (SEQ ID NO:4) were used, and resulted in the synthesis of a fragment of the correct size (934 bp). The amplified product was subcloned in the *Hin*cII site of the plasmid pT7T3-18U (Pharmacia) to produce plasmid pT7T3-18U/proFAE900, followed by complete sequence determination of both strands to verify the fragment identity. A BLAST search of the *A. thaliana* Database identified a single BAC clone T4L20 (GenBank ATF10M6) 125,179 bp long, which contains the complete *FAE1* gene.

The paragraph commencing at page 12, line 18 is amended as follows:

Construction of the vectors pFAE900-GUS and pFAE400-GUS, and transformation of *Arabidopsis* and tobacco, was as follows. The insert was cleaved out of pT7T3-18U vector with *Hin*dIII and *Xba*I and directionally subcloned into the corresponding sites of the binary Ti plasmid pBI101 (Clontech), which contains a promoterless GUS gene (Jefferson et al. 1987), to obtain the vector pFAE900-GUS. Another construct, pFAE400-GUS, containing only 393 bp of the 5' *FAE1* region directly upstream of the ATG initiation codon (SEQ ID NO:15) fused to the GUS coding sequence was also generated. For that, the pT7T3-18U/proFAE900 vector was digested with *Bg1II* and *PstI*, the sticky ends were filled in using T4 DNA polymerase, followed by re-ligation to obtain pT7T3-18U/proFAE400. The 393 bp 5' *FAE1* upstream fragment was then excised with *Hin*dIII and *Xba*I and cloned into the binary vector pBI101 to obtain the plasmid pFAE400-GUS. The pFAE400-GUS and pFAE900-GUS fusion constructs in pBI101 were introduced into *Agrobacterium tumefaciens* strain GV3101 (Koncz and Schell, 1986) by heat-shock and selected for resistance to kanamycin (50 µg/ml). *A. thaliana* (L.) Heynh. ecotype Columbia was transformed with the pFAE400-GUS and pFAE900-GUS constructs using floral dip method (Clough and Bent, 1998). Screening for transformed seed

The partial paragraph at page 15, lines 1-10 is amended as follows:

cutting restriction enzymes (*DraI, EcoRV, HpaI, PvuII and ScaI*) to generate a series of DNA libraries. After ligation of adapter molecules, individual libraries were used as templates in a two step PCR. In the first PCR amplification using the AP1 primer 5'-GGATCCTAATACGACTCACTATAGGGC-3' (SEQ ID NO:5) and the *FAE1* gene specific primer 5'-AAAGAGTGGAGCGATGGTTATGAGG-3' (SEQ ID NO:6) (Bnwalk1), multiple DNA fragments were amplified from all five library templates. After a second round of PCR, using the AP2 primer 5'-CTATAGGGCTCGAGCGGC-3' (SEQ ID NO:7) and the nested *FAE1* specific primer 5'-CGGAAAGAAGCAAAGGTTGAAAAGG-3' (SEQ ID NO:8) (Bnwalk2), the longest single fragment of 1.6 kb was obtained from the *HpaI* library template. This fragment was inserted into the pCR2.1 plasmid (Invitrogen) and sequenced. The sequence is shown in Figure 2.

The paragraph commencing at page 15, line 11 is amended as follows:

For the PCR walking experiment to isolate the *L. annua* 5' regulatory region, in addition to the standard AP1 and AP2 primers, the following *FAE1* specific primers were used: 5'-

GATCGTTTGTGGTAAGACGAGAGC-3' (SEQ ID NO:9) (Lawalk1) and 5'-GTCAGTGGGAAGAAACAGAGGTTG-3' (SEQ ID NO:10) (Lawalk2). In the first PCR reaction, the *DraI, EcoRV, PvuII, ScaI* and *SspI* library templates were used. In a second PCR amplification the longest single fragment 1.1 kb in length was synthesized using the *EcoRV* library template. This fragment was inserted into the *HincII* site of the pT7T3-18U vector (Promega), sequenced on both strands and analyzed (Figure 3).

The paragraph commencing at page 15, line 19 is amended as follows:

Using the sequence data obtained for the 5' regulatory regions generated by PCR walking, specific primers were generated for the amplification of the *L. annua* and *B. napus FAE1* promoter fragments. For the PCR-amplification of *B. napus* promoter fragment the upstream primer was 5'-CTGACTTCACCAAAGAAACAACTCG-3' (SEQ ID NO:11) (BnproFW) in combination with the downstream primer 5'-CGGAATTCCGTTTTTTTTTTTAGGCG-3' (SEQ ID NO:12) (BnproRV). The synthesized fragment was ligated into the *SmaI* site of pGEM-7Zf (Promega), then excised with *XbaI/BamHI* and cloned into the equivalent sites of the pBI101 binary vector (Clontech). *L. annua* 5' regulatory region was amplified using the 5'-CAGCTTAACCGGTAAAATTGGCC-3' (SEQ ID NO:13) (LaproFW) upstream primer together with the 5'-TGTTCAGTTTTGTGTCGGAGAGG-3' (SEQ ID NO:14) (LaproRV) downstream primer and inserted in the *HincII* site of pT7T3-18U (Promega) plasmid. In order to clone the *L. annua* promter fragment into the pBI101 binary vector, an *XbaI* site was added by subcloning the *PstI/KpnI* fragment released from the pT7T3-18U vector into pBluescript II KS+ (Stratagene). The fragment was then excised and cloned in the *XbaI* site of the pBI101 vector.

In the Claims:

New claims 29-38 are added.

Claims 1 and 19 have been amended as follows:

1. (Amended twice) A recombinant nucleic acid molecule comprising a heterologous promoter sequence operably linked to a nucleic acid sequence, wherein the promoter sequence comprises a transcriptional regulatory region capable of [mediating] directing seed-specific expression in *Arabidopsis* wherein the transcriptional regulatory region hybridizes under

stringent conditions to a sequence selected from the group consisting of SEQ ID NO:15, 16 , 17, and 18, or the complement thereof.

19. (Amended twice) A method of altering the phenotype of a seed comprising:

a) transforming a seed-bearing plant, or a progenitor of a seed-bearing plant, with a vector comprising the nucleic acid molecule of claim 1; and

b) growing the seed-bearing plant to obtain seed [under conditions] wherein the nucleic acid sequence is expressed during embryogenesis under control of the transcriptional regulatory region to alter the phenotype of the seed.